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; FEATURE:
; OTHER INFORMATION: Synthetically derived DNA
US-09-164-249B-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chetverin, Alexander B.
APPLICANT: Kramer, Fred Russel
TITLE OF INVENTION: NOVEL OLIGONUCLECTIDE ARRAYS AND THEIR USE FOR SORTING,
TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS
FILE REFERENCE: 07763-004003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Patent No. 6322971
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PRIOR FILING DATE: 1992-02-19
NUMBER OF SEQ ID NOS: 18
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PRIOR APPLICATION NUMBER: US 08/473,010
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/247,530
PRIOR APPLICATION NUMBER: US 08/247,530
PRIOR APPLICATION TUBER: 1994-05-23
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APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ily.
APPLICANT: Blumenfeld, M
                                                                                                                                                                                                   APPLICANT: Chumakov, Ilya
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate cancer gene
NUMBER OF SEQUENCES: 68
CORRESPONDENCES: 68
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
                                                                                                                                                                                  ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
            OPERATING SYSTEM: Win95
SOFTWARE: Word
                                                                                                                           CITY: San Diego
STATE: California
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                                                                                                                    COUNTRY:
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US-09-042-225-4
US-09-390-324B-1
US-10-015-593-1
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Pred. No. 41;
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US-08-430-536A-2
US-08-684-547-2
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PEATURE: misc feature
IOCATION: 1..24
IOTHER INFORMATION: primer oligonucleotide PGRT32
US-09-338-907-10
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EARLIER APPLICATION NUMBER: 08/996,306
EARLIER FILING DATE: 1997-12-2
EARLIER APPLICATION NUMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-12-22
NUMBER: 0F SEQ ID NOS: 578
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Matches
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SEQ ID NO 10
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Best Local S
                                                                 Matches
                                                                                 Query Match
Best Local :
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET.18CP1CP
CURRENT APPLICATION NUMBER: US/09/338,907
                                                                                                                                                                                                                LENGTH: 24
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ISTRAESED, Ned A,
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PGRT32
LOCATION: complement 5198..5221
OTHER INFORMATION: Location relative to seqID3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 24 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                              1732 ТТАСАЛАЛАЛАЛАЛАЛАЛАЛ 1754
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                                                                 Conservative
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Pred. No. 57;
                                                               0; Mismatches
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                                                                                 Score 21.4;
Pred. No. 57
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Sequence 55, Appl 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000-55 1000
Section Sect
76.6 12.4 0.7 14 1 US-08-832-021-8 Sequence 76.6 12.4 0.7 14 1 US-08-832-021-8 Sequence 76.6 12.4 0.7 14 1 US-08-832-021-8 Sequence 76.6 12.4 0.7 14 1 US-08-832-021-12 Sequence 76.6 12.4 0.7 14 1 US-08-832-021-12 Sequence 76.6 12.4 0.7 14 1 US-08-832-021-12 Sequence 76.6 12.4 0.7 14 1 US-08-832-021-13 Sequence 76.6 12.4 0.7 14 1 US-08-724-668-17 Sequence 77.1 12.4 0.7 14 1 US-08-724-668-17 Sequence 77.1 12.4 0.7 14 1 US-08-724-668-20 Sequence 77.1 12.4 0.7 14 1 US-08-724-668-20 Sequence 77.1 12.4 0.7 14 1 US-08-822-660-16 Sequence 77.1 12.4 0.7 15 1 US-08-822-600-16 Sequence 77.1 12.4 0.7 15 1 US-08-822-621-19 Sequence 77.1 12.4 0.7 15 1 US-08-822-621-14 Sequence 87.1 12.4 0.7 15 1 US-08
12.4 0.7 14 1 US-08-832-021-8 Sequence 12.4 0.7 14 1 US-08-832-021-8 Sequence 12.4 0.7 14 1 US-08-832-021-12 Sequence 12.4 0.7 14 1 US-08-832-021-12 Sequence 12.4 0.7 14 1 US-08-734-4668-16 Sequence 12.4 0.7 14 1 US-08-734-4668-17 Sequence 12.4 0.7 14 1 US-08-734-4668-19 Sequence 12.4 0.7 14 1 US-08-892-1640-19 Sequence 12.4 0.7 14 1 US-09-303-069-10 Sequence 12.4 0.7 15 US-09-303-069-
7 14 1 US-08-832-021-8 Sequence 7 14 1 US-08-832-021-11 Sequence 7 14 1 US-08-832-021-12 Sequence 7 14 1 US-08-832-021-12 Sequence 7 14 1 US-08-832-021-12 Sequence 7 14 1 US-08-724-466B-16 Sequence 7 14 1 US-08-724-466B-16 Sequence 7 14 1 US-08-724-466B-16 Sequence 7 14 1 US-08-724-466B-19 Sequence 7 14 1 US-08-724-466B-19 Sequence 7 14 1 US-08-724-466B-19 Sequence 7 14 1 US-08-821-164D-16 Sequence 7 14 1 US-08-821-164D-16 Sequence 7 14 1 US-08-821-164D-16 Sequence 7 14 1 US-08-821-164D-17 Sequence 7 14 1 US-08-821-164D-18 Sequence 7 14 1 US-08-821-164D-19 Sequence 7 14 1 US-08-832-164D-19 Sequence 7 14 1 US-08-832-164D-19 Sequence 7 14 1 US-08-831-255-13 Sequence 7 14 1 US-08-831-255-13 Sequence 7 14 1 US-08-831-255-13 Sequence 7 15 1 US-08-832-021-18 Sequence 7 15 1 US-08-832-021-19 Sequence 7 15 1 US-08-832-021-19 Sequence 7 15 1 US-08-832-021-46 Sequence 7 15 1 US-08-832-021-47 Sequence 7 15 1 US-08-832-021-47 Sequence 7 15 1 US-08-832-021-47 Sequence 7 15 1 US-08-832-021-48 Sequence 7 15 1 US-08-832-021-49 Sequence 7 15 1 US-08-832-021-49 Sequence 8 15 1 US-08-832-021-49 Sequence 8 15 1 US-08-832-021-49 Sequence 8 15 1 US-08-832-021-49 Sequence 9 15 1 US-08-832-021-59 Sequence 9 15 1 US-08-832-
1 US-08-832-021-7 US-08-832-021-1 Sequence 1 US-08-832-021-1 Sequence 1 US-08-832-021-1 Sequence 1 US-08-832-021-1 Sequence 1 US-08-724-466B-16 Sequence 1 US-08-724-466B-20 Sequence 1 US-08-724-466B-20 Sequence 1 US-08-724-466B-20 Sequence 1 US-08-724-466B-20 Sequence 1 US-08-82-164D-16 US-08-82-164D-17 US-08-82-164D-17 US-08-82-164D-18 Sequence 1 US-08-82-164D-19 US-08-82-164D-20 Sequence 1 US-08-82-164D-19 US-08-83-164D-20 US-08-83-164D-20 US-08-83-164D-20 US-08-83-021-4 US-08-83-021-4 US-08-33-021-4 US-08-33-021-4 US-08-33-021-4 US-08-33-021-4 US-08-33-021-4 US-08-33-021-4 US-08-33-021-4 US-08-83-021-4 US-08-8
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   Litfin M,
   Schneider S;
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A genetically modified glucocorticoid receptor which is transactivation deficient is used to identify cofactors which will be useful to provide inflammation-inhibiting and immunosuppressive treatment.

Disclosure; Col 12; 12pp; German

ABX94934/c

ABX94934;

XX

ABX94934;

XX

DET 25-AUG-2003 (first entry)

XX

Remilla luciferase associated

XX

Luciferase; ubiquitin promote

XX

Luciferase; ubiquitin promote

XX

DE10222714-A1.

XX

DE10222714-A1.

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DE10222714-A1.

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PP 23-MAY-2002; 2002DE-01022714.

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C2-JAN-2003.

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28-MAY-2001; 2001DE-01022714.

XX

A genetically modified glucoc

DET 2003-291460/29.

XX

Disclosure; Col 12; 12pp; Ger

XX

Cranstruct comprising at least

CC construct which an expression

CC construct with an expression

CC gene encoding a cofactor in the

CC construct with an expression

CC preferably a DNA-binding dome

CC preferably a DNA-binding dome

CC construct with an expression

CC prespector and (c) isolatin

CC construct with an expression

CC preferably a DNA-binding dome

CC prespector and (c) isolatin

CC protein-protein interaction in

CC protein-protein interaction

CC protein-protein interaction

CC protein-protein omplex binding

CC dad (6) a compound with an in

CC protein-protein complex binding

CC protein-protein complex binding

CC protein-protein omplex binding

CC protein-protein ompl CC This invention describes a novel genetically modified glucocorticoid corrector, which has transrepression protein-protein reciprocal effects construct comprising at least a nucleic acid encoding the glucocorticoid corrector, operably linked with regulatory sequences of a reporter gene, construct comprising at least an uncleic acid encoding the glucocorticoid receptor, operably linked with regulatory sequences of a reporter gene, corrector, operably linked with regulatory sequences of a reporter gene, corrector, operably a DNA-binding domain for a reporter gene; (2) identifying a cofactor involved in glucocorticoid receptor modulation of at least another transcription factor comprising; (a) using the above construct with an expression bank of a eukaryotic cell expressed in a corrector two hybrid system; (b) detecting a specific protein complex or the receptor and a cofactor through growth in a selective medium for the receptor and a cofactor through growth in a selective medium for the reporter and (c) isolating and characterising the nucleic acid corresponding the cofactor in the cDNA clone; (3) a cofactor which in a protein-protein interaction achieves a reciprocal effects whereby within a distribution of the protein partner is measured by expression of the receptor with other transcription construer is measured by expression of the receptor with other transcription construct is contacted by expression of the reporter gene or detecting partner is measured by expression of the interaction of the protein protein compune with an inflammation-inhibiting or immunosuppressive exteatment. This sequence represents a pck primer #198rev used to amplify a Renilla confidence in inflammation inhibiting or immunosuppressive treatment. behind a ubiquitin promoter

Sequence 27 BP; 5 A; 6 C; 11 G; 5 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; 1.5%; Score 27; DB 1; Length 27; Pred. No. 23;

AND	
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Human zsig63 PCR/s
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1 (bases 1 to 24)

1 (bases 1 to 24)

Chetverin, A.B. and Kramer, F.R.

Oligonucleotide arrays and their use for sorting, isolating, only only only one of the sequencing, and manipulating nucleic acids sequencing, and manipulating nucleic acids patent: US 6322971-A 6 27-NOV-2001;
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26; Conserv
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1 (Dases 1 to 29)

Szalai,C., Toth,S. and Falus,A.

Exon-intron organization of the human gpl30 gene

Gene 243 (1-2), 161-166 (2000)

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